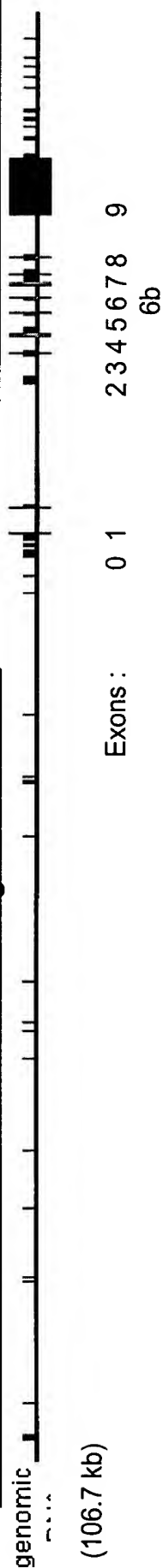


# Localisation of non-exonic SNPs on the genomic DNA:



# Localisation of exonic SNPs on one of the three alternative forms:

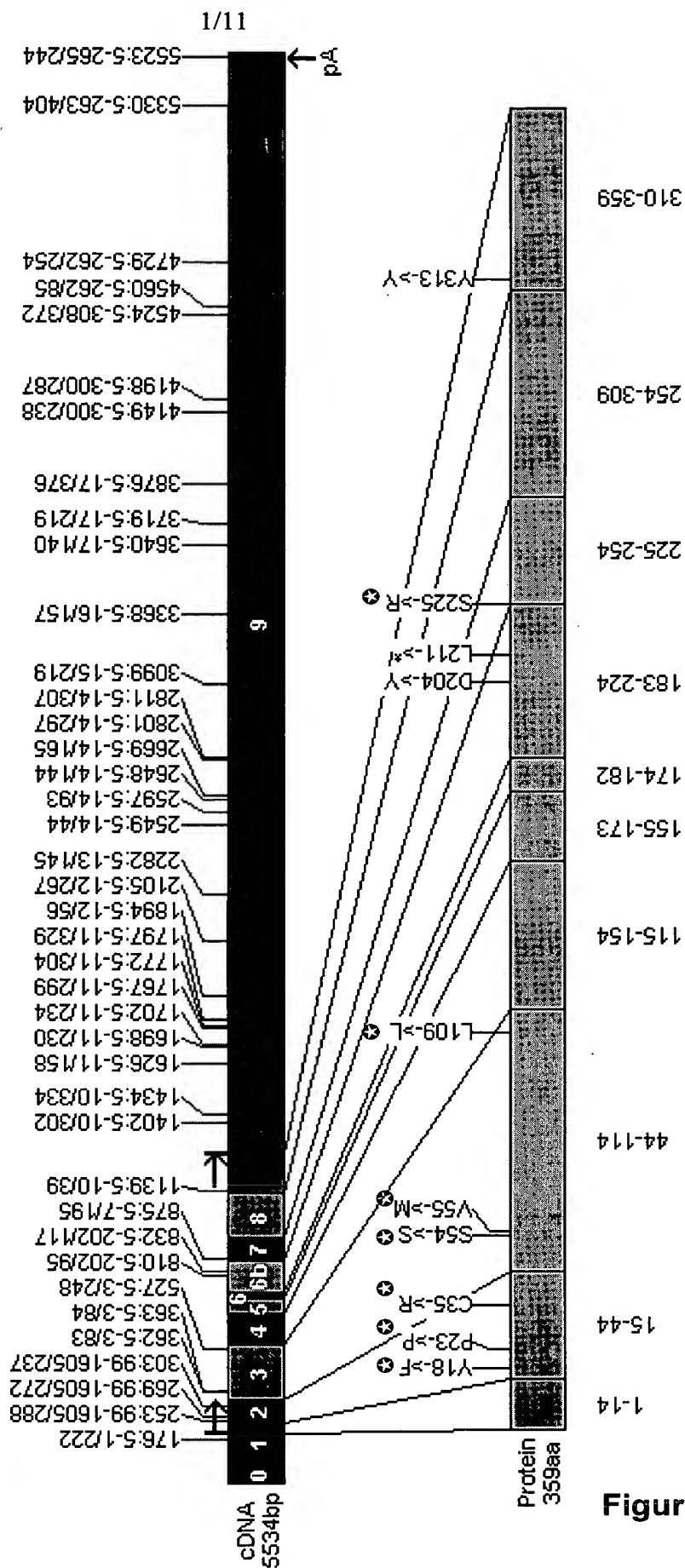


Figure 1A

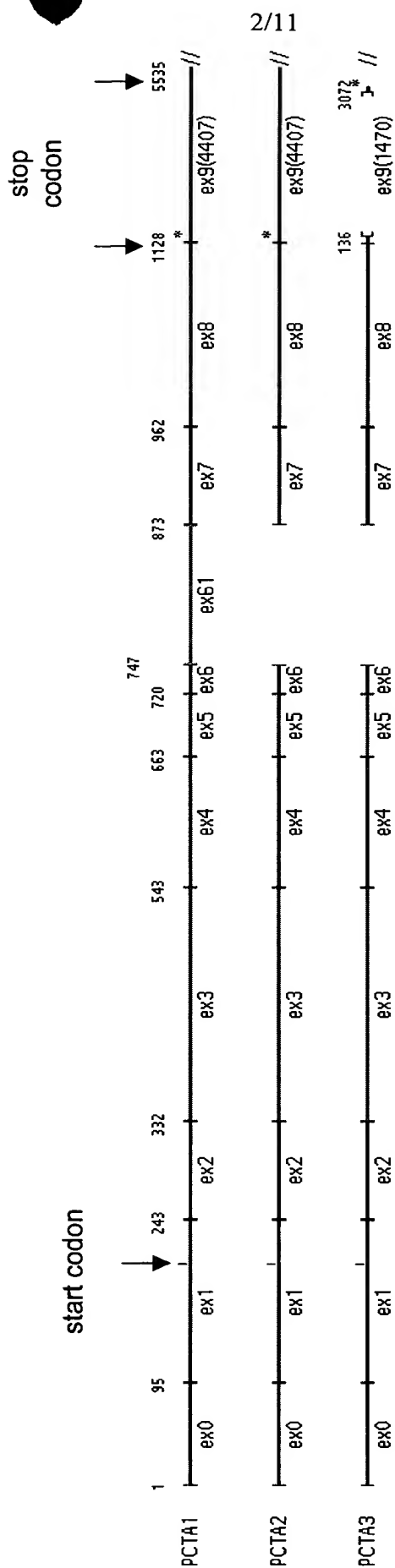


Figure 1B

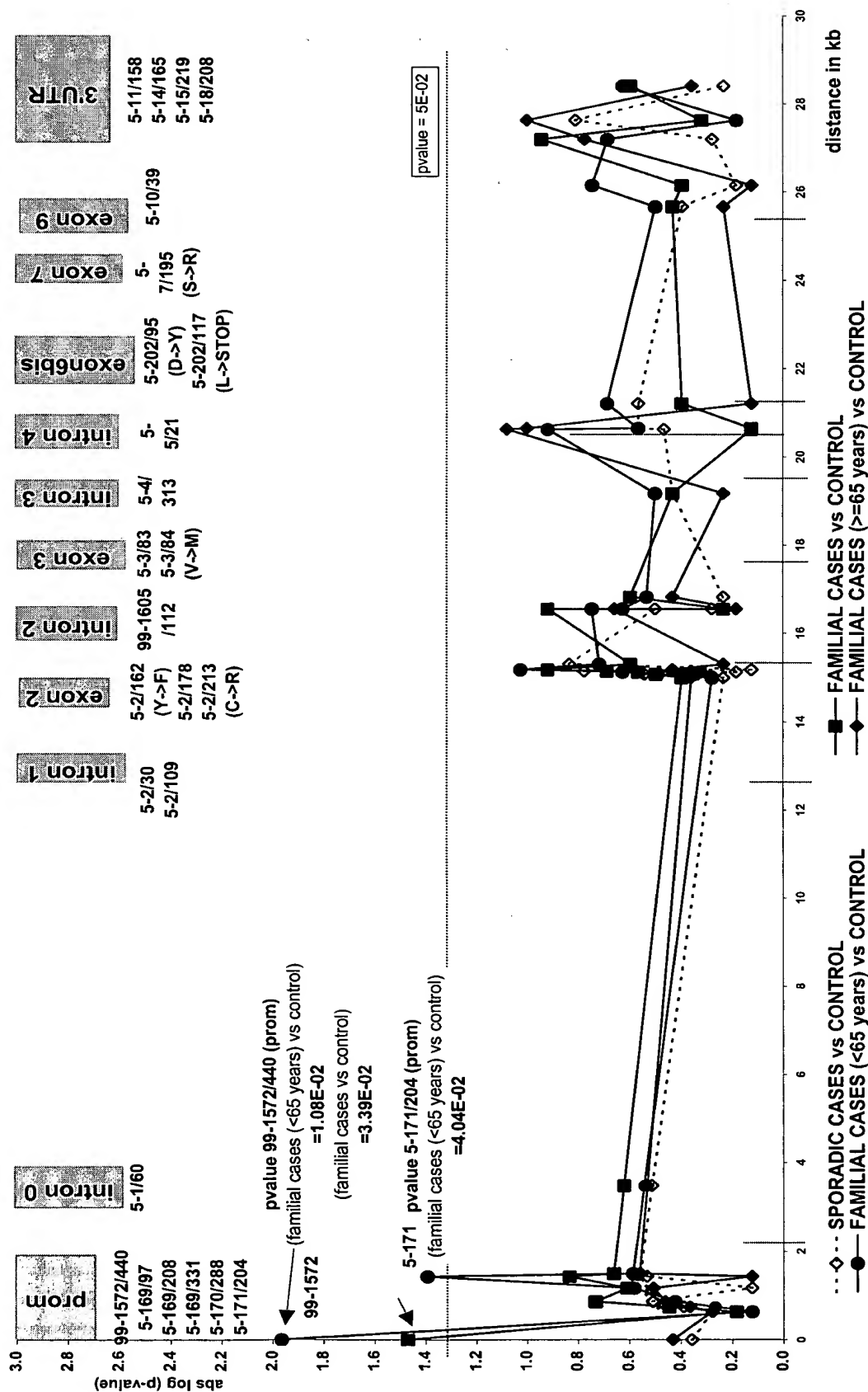


Figure 2

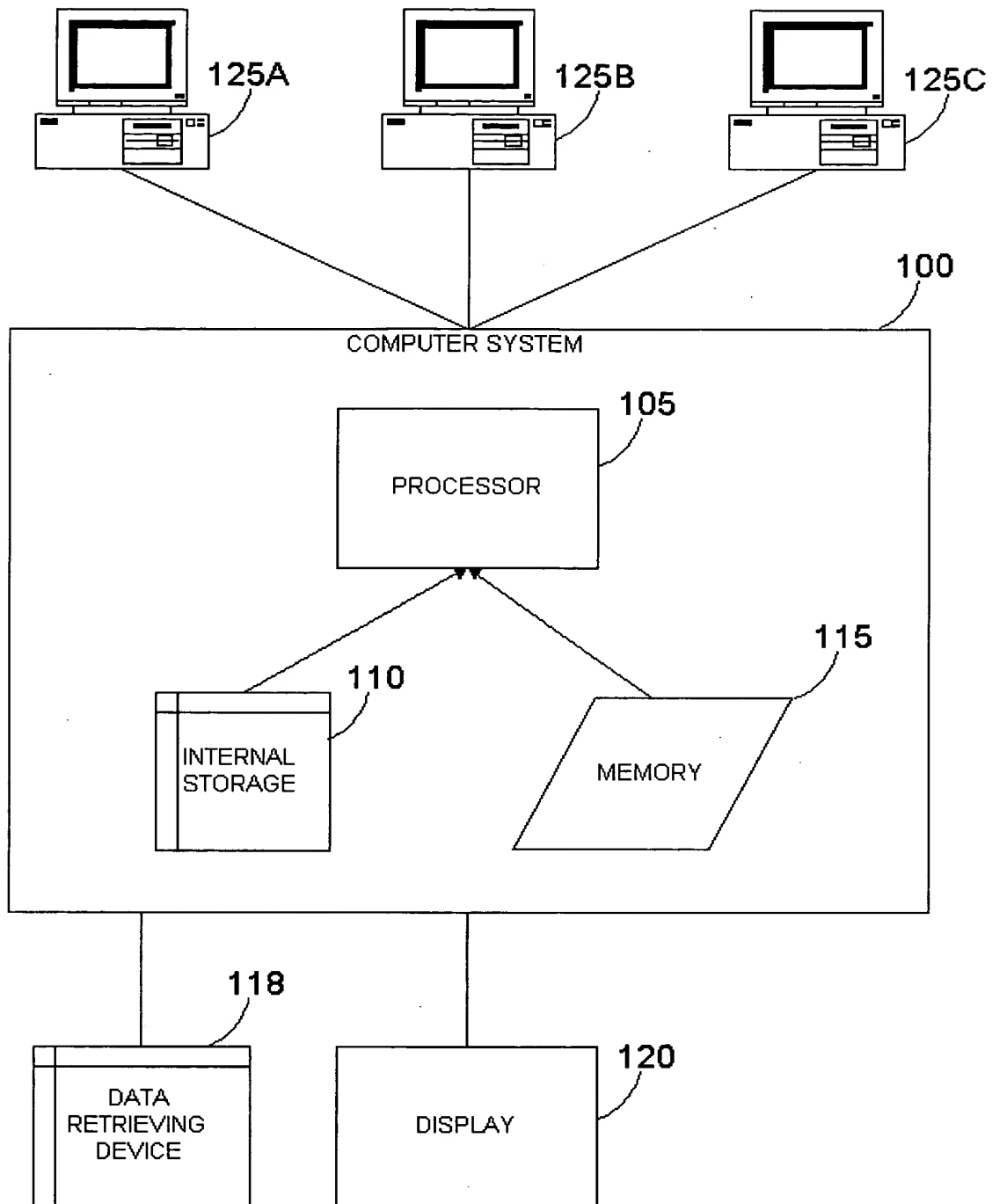


Figure 3

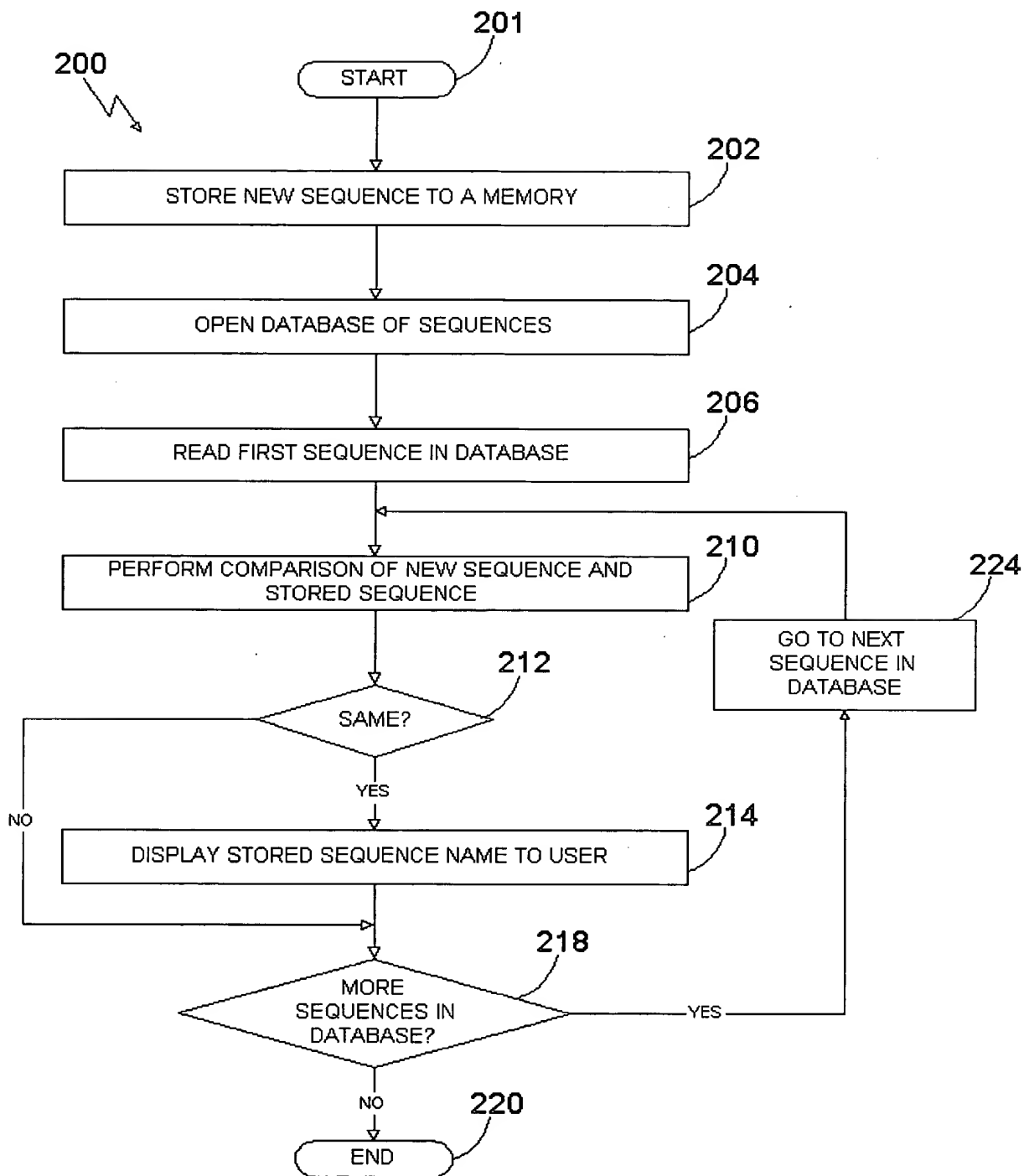


Figure 4

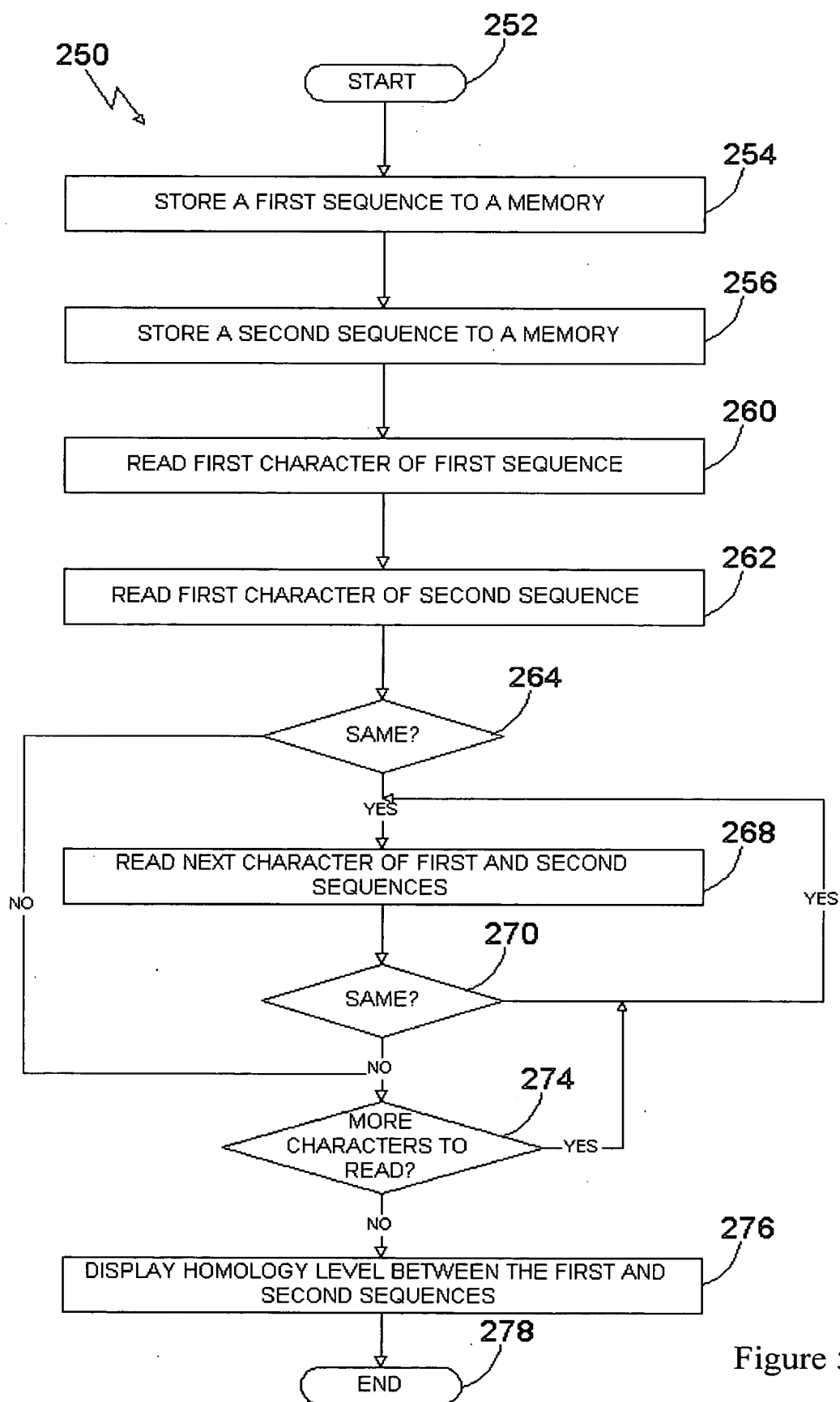


Figure 5

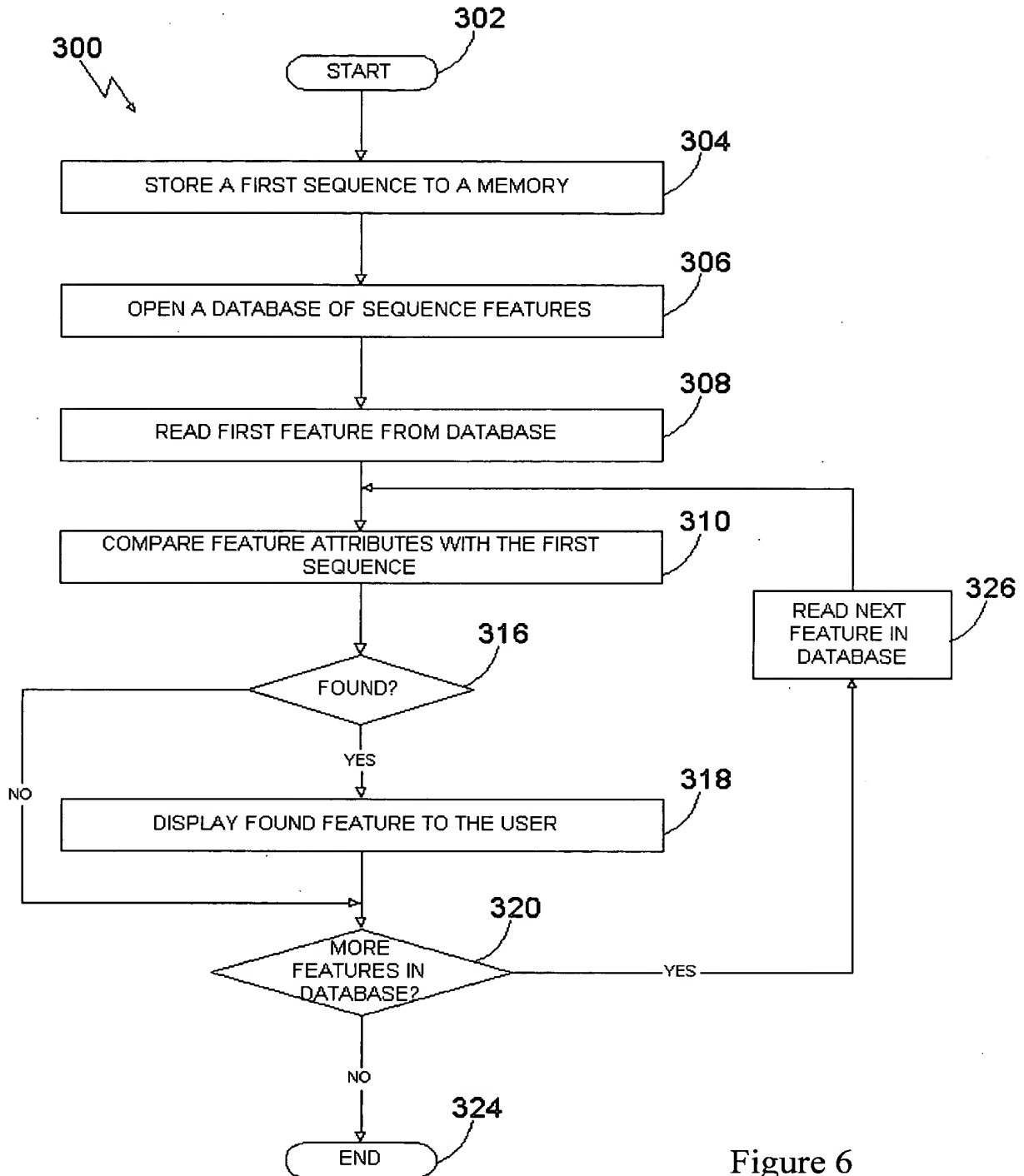


Figure 6

FIGURE 7A

	1				50
leg2	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
leg1	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
PCTA	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
PCTA.var	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
PCTA.mus	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
gal9-1	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
gal	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
leg7	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
gal4	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
Consensus	-----	-----	-----	-----	-----
	51				100
leg2	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
leg1	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
PCTA	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
PCTA.var	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
PCTA.mus	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
gal9-1	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
gal	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
leg7	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
gal4	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~M
Consensus	-----	-----	-----	-----	-----
	101				150
leg2	~~~~~	~~~~~MTGELE	VKNMDMKPGS	TLKITGSIAD	.GTDGFFVINL
leg1	~~~~~	~~~~~ACGLV	ASNLNLKPGE	CLRVRGEVAP	.DAKSFVLNL
PCTA	MLSLNNLQNI	IYNPVIPIYVG	TIPDQLDPGT	LIVICGHV.P	SDADRFQVDL
PCTA.var	MLSLNNLQNI	IYNPVIPIYVG	TIPDQLDPGT	LIVICGHV.P	SDADRFQVDL
PCTA.mus	MLSLNNLQNI	IYNPIIPYVG	TITEQLKPGS	LIVIRGHV.P	KDSERFQVDF
gal9-1	~MAFSGSQAP	YLSPAVPFSG	TIQGGLQDGL	QITVNGTVLS	SSGTRFAVNF
gal	~MAFSGSQAP	YLSPAVPFSG	TIQGGLQDGL	QITVNGTVLS	SSGTRFAVNF
leg7	~~~~~	~~~~~SNVPHKS	SLPEGIRPGT	VLRIRG.LVP	PNASRFHVN
gal4	AYVPAPGYQP	TYNPTLPYYQ	PIPGGLNVGM	SVYIQG.VAS	EHMKRFFVNF
Consensus	-----	---P--P---	-IP-GL-PG-	---I-G-V-P	--A-RF-VNL

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FIGURE 7B

	151				200
leg2	GQGTD.....	KLNLHFNPRF	S....ESTIV	CNSLDGSM	
leg1	GKDSN.....	NLCLHFNPRF	NAHGDANTIV	CNSKDGGG	
PCTA	QNGSSVKPRA	DVAFHFNPRF	K.RAGC..IV	CNTLINEE	
PCTA.var	QNGSSVKPRA	DVAFHFNPRF	K.RAGC..IV	CNTLINEE	
PCTA.mus	QLGNSLKPRA	DVAFHFNPRF	K.RSSC..IV	CNTLTQEE	
gal9-1	QTGFS...GN	DIAFHFNPRF	E.DGGY..VV	CNTRQNGS	
gal	QTGFS...GN	DIAFHFNPRF	E.DGGY..VV	CNTRQNGS	
leg7	LCGEE..QGS	DAALHFNPRF	D..TSE..VV	FNSKEQGS	
gal4	VVGQD..PGS	DVAFHFNPRF	D.GWDK..VV	FNTLQGGKWG	SEERKRSMPP
Consensus	--G-----G-	D-AFHFNPRF	-----VV	CNT---G-WG	-EER----PF
	201				250
leg2	SPGSEVKFTV	TFESDKFKVK	LPDGHELTFF	NRLG.HSHLS	YLSVRGGFNM
leg1	QPGSVAEVC	TFDQANLTVK	LPDGYEFKFP	NRLN.LEAIN	YMAADGDFKI
PCTA	KREKSFEIVI	MVLKDKFQVA	VNGKHTLLYG	HRI.GPEKID	TLGIYGVNI
PCTA.var	KREKSFEIVI	MVLKDKFQVA	VNGKHTLLYG	HRI.GPEKID	TLGIYGVNI
PCTA.mus	RREKSFEIVF	MVLKNKFQVA	VNGRHVLLYA	HRI.SPEQID	TVGIYGVNI
gal9-1	QKGMPFDLCF	LVQSSDFKVM	VNGILFVQYF	HRV.PFHRVD	TISVNGSVQL
gal	QKGMPFDLCF	LVQSSDFKVM	VNGILFVQYF	HRV.PFHRVD	TIFVNGSVQL
leg7	QRGQPFEVLI	IASDDGFKAV	VGDAQYHHFR	HRL.PLARVR	LVEVGGDVQL
gal4	KKGAAPFELV	IVLAEHYKVV	VNGNPFYEY	HRL.PLQMT	HLQVDGDLQL
Consensus	--G--FE---	-V--D-FKV-	VNG-----Y-	HRL-PL--V-	---V-GDVQL
	251				300
leg2	SSFKLKE~~~	~~~~~	~~~~~	~~~~~	~~~~~
leg1	KCVAFD~~~~	~~~~~	~~~~~	~~~~~	~~~~~
PCTA	HSIGFSFSSD	LQSTQASSLE	LTEISRENV	KSGTPQL...	.....
PCTA.var	HSIGFSFSSD	LQSTQASSLE	LTEISRENV	KSGTPQLPSN	RGGDISKIAP
PCTA.mus	HSIGFRFSSD	LQSMETSALG	LTQINRENI	KPGKLQL...	.....
gal9-1	SYISFQNPRT	VPVQPAFSTV	PFSQPVCPPP	RPRGRRQKPP	GVWPANPAPI
gal	SYISFQ....	.....	.....	.....PP	GVWPANPAPI
leg7	DSVRIF~~~~	~~~~~	~~~~~	~~~~~	~~~~~
gal4	QSINFI....	.....	.....	.....GGQP	.LRPQGPPMM
Consensus	-SI-F-----	-----	-----	-----	-----

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FIGURE 7C

	301				350
leg2	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
leg1	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
PCTA	.....	.....	.....S	..LPFAARLN	TPMGPGRTVV
PCTA.var	RTVYTKSKDS	TVNHTLTCTK	IPPMNYVSKS	..LPFAARLN	TPMGPGRTVV
PCTA.mus	.....	.....	.....S	..LPFEARLN	ASMGPGRITVV
gal9-1	TQTVIHTVQS	APGQMFSTPA	IPPMYHPHA	YPMPFITLIL	GGLYPSKSIL
gal	TQTVIHTVQS	APGQMFSTPA	IPPMYHPHA	YPMPFITLIL	GGLYPSKSIL
leg7	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
gal4	PPYPGPGHCH	QQLNSLPTME	GPPTFNP...	.PVPYFGRLQ	GGLTARTII
Consensus	-----	-----	-----	---P---	-----

	351				400
leg2	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
leg1	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
PCTA	VKGEVNANAK	SFNVDLLAGK	SKDIALHLNP	RLNIKAFVRN	SFLQES
PCTA.var	VKGEVNANAK	SFNVDLLAGK	SKDIALHLNP	RLNIKAFVRN	SFLQES
PCTA.mus	IKGEVNTNAR	SFNVDLVAGK	TRDIALHLNP	RLNVKAFVRN	SFLQDA
gal9-1	LSGTVLPSAQ	RFHIN..LCS	GNHIAFHLNP	RFDENAVVRN	TQIDNS
gal	LSGTVLPSAQ	RFHIN..LCS	GNHIAFHLNL	RFDENAVVRN	TQIDNS
leg7	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
gal4	IKGYVPPTGK	SFAINFKVG	SGDIALHINP	RMGNGTVVRN	SLLNGS
Consensus	--G-V----	-F-----	---IA-H-N-	R-----VRN	-----WG-E

	401				450
leg2	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
leg1	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
PCTA	SPGMYFEMII	YCDVREFKVA	VNGVHSLEYK	HRFKELSSID	
PCTA.var	SPGMYFEMII	YCDVREFKVA	VNGVHSLEYK	HRFKELSSID	
PCTA.mus	SSGMYFEMII	YCDVREFKVA	INGVHSLEYK	HRFKDLSSID	
gal9-1	VRGQSFSVWI	LCEAHCLKVA	VDGQHLFEYY	HRLRNLPITN	
gal	VRGQSFSVWI	LCEAHCLKVA	VDGQHLFEYY	HRLRNLPITN	
leg7	~~~~~	~~~~~	~~~~~	~~~~~	
gal4	GPGQFFDLIS	RCGLDRFKVY	ANGQHLFDFA	HRLSAFQRVD	
Consensus	E-----PF	--G--F---I	-C-----KV-	--G-H-----	HR-----

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FIGURE 7D

	451	466
leg2	~~~~~	~~~~~
leg1	~~~~~	~~~~~
PCTA	TLEINGDIHL	LEVRSW
PCTA.var	TLEINGDIHL	LEVRSW
PCTA.mus	TLSDVDGDIRL	LDVRSW
gal9-1	RLEVGGDIQL	THVQT~
gal	RLEVGGDIQL	THVQT~
leg7	~~~~~	~~~~~
gal4	TLEIQGDVTL	SYVQI~
Consensus	-L---GD--L	--V---

■ Galactoside binding site

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